

Fig. 1

Fig 2

HIP1 Clones: Nucleotide Alignment

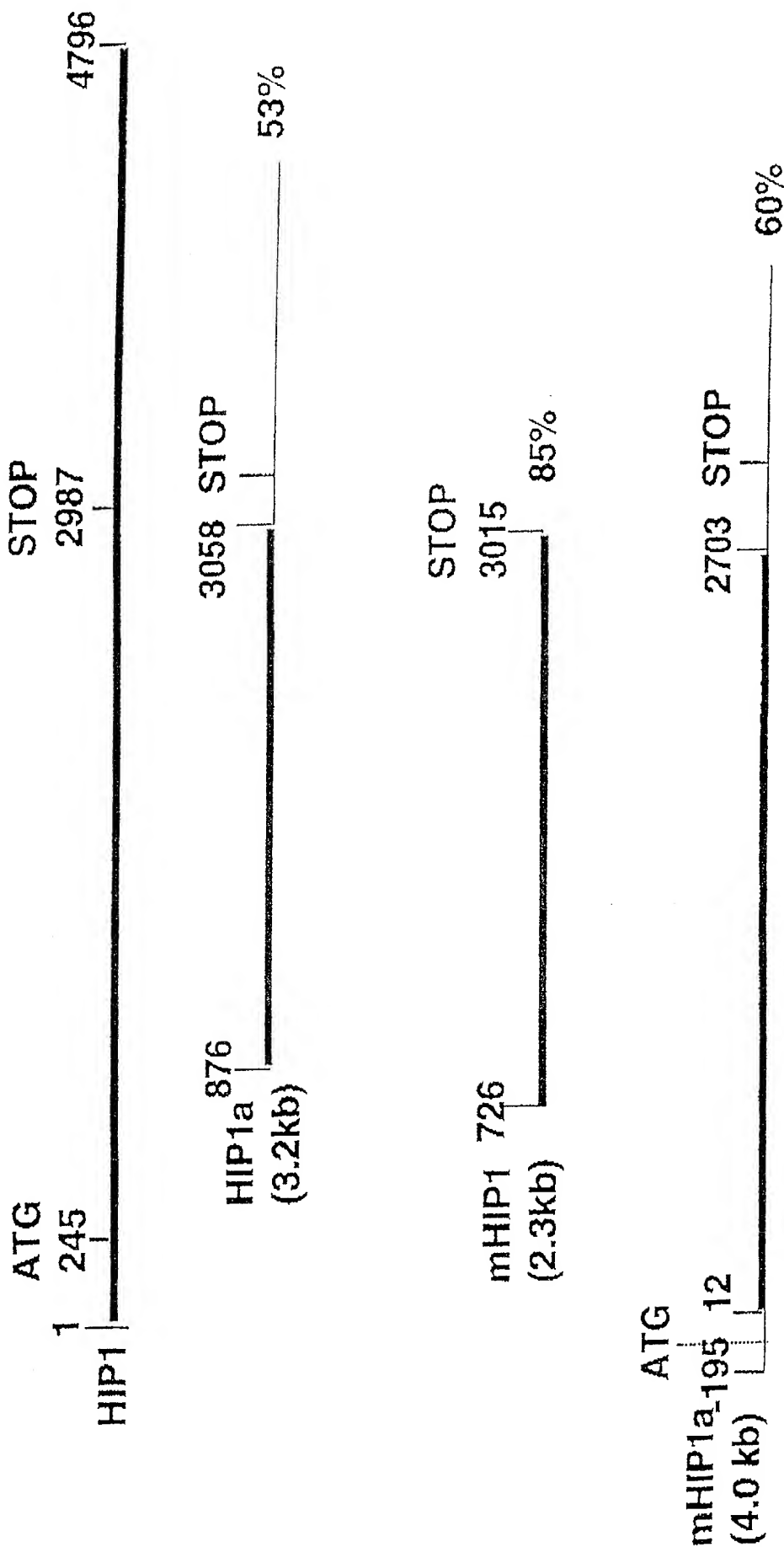


Fig 3
HIP1 Clones: Protein Alignment

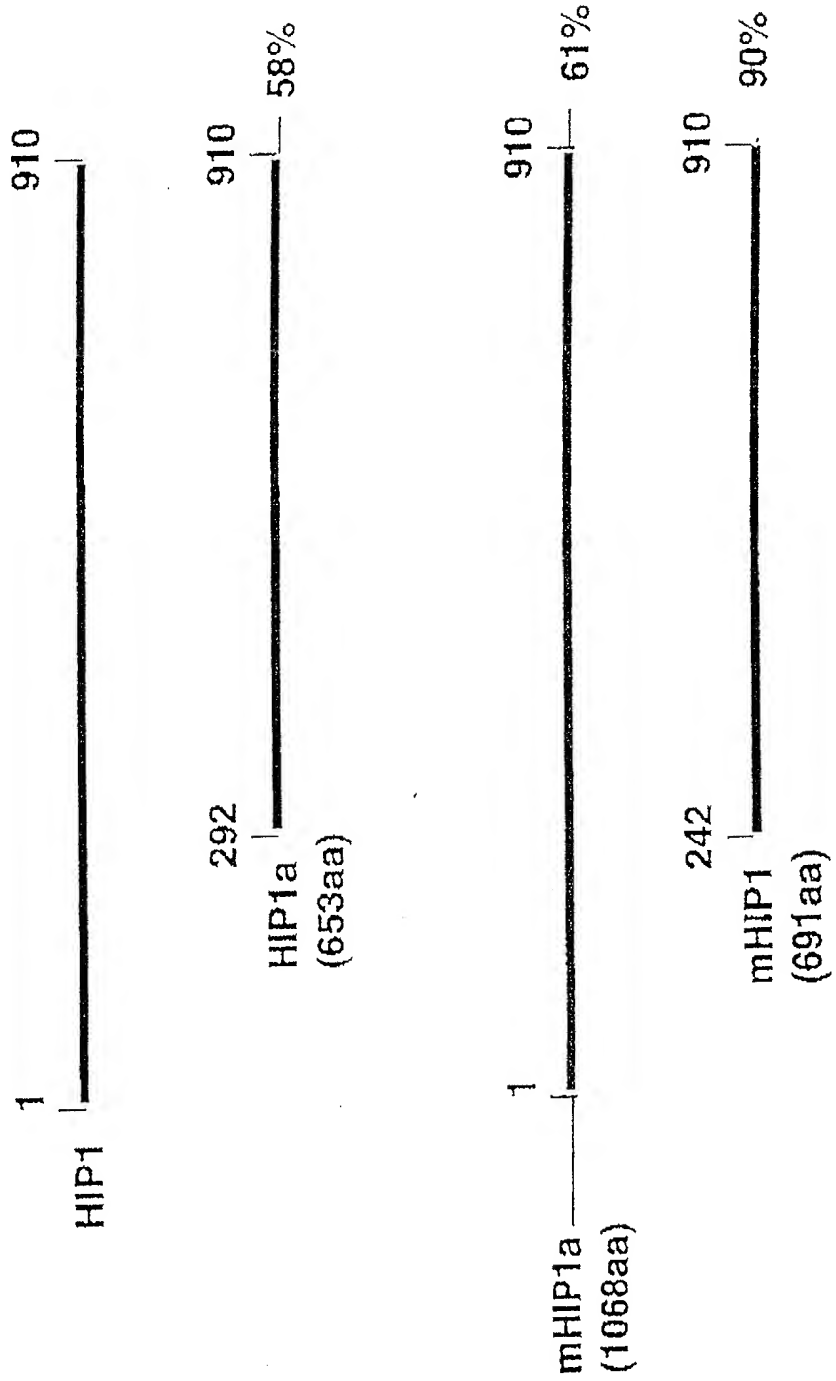


Fig 4

>Usurpin A
SAEVIHQVEEALDTDEKKMLLFLCRDVAIDVVPNVRDLDILRERGLSVCDLAEELLYRVHRFDLLKRILK

>Usurpin B
YRVLMAHIGEDLDKSDVSSLIFLMKDYMGGRGKISKHKSFLLVVELHKLNLVAPDQDLLEKCLKNHRIDLKTKIQK

>Casp-8 A
FSRNLYDIGELQDSEDLASLKELSLDYIPQRKOEPIKDALMIFQRLOEKRMLEESNLSFLKELLFRINRLDLLITYLN

>Casp-8 B
YRVMLYQISEEVSREELRSFKFLQHEISKCKLODDMNLLDIFIEMEKRVILGEGKLDILKRVCAQINKSLLKIND

>Casp-10 A
FRHKLLTIDSNLGVQDVENLKFLCIGLVPNKKLEKSSSASDVFEHLLANDLLSEEDPPFLAEELLYIIRQKKLLQHLNC

>Casp-10 B
FRNLLYELSEGIDSENKDMIFLLKDSLPKTEMTSLSFLEKQKIDEDNLTCLDLCKTVVPKLLRNIEK

>FADD
FLVLLHSVSSSLSSSELTFLKFLCGRVGKRLKERVQSGLDLFSMLLEQNDLEPGHTELLRELLASLRNDLLRRVDD

>MC159 A
SLPFLRHLLLEELDSHEDSLLLFLGHDAAPGCTTVTQALCSLSQQRKLTAAALVEMLYVLQRMDDLKSRFG

>MC159 B
YHKLMVCVGEELDSSSELRALRLFACNLNPSLSTALSESSRPVELVLALENVGLVSPSSSVLADMLRTLRRDLDCQQLVE

>E8
FRCLMALVNDFLSDKEVEEHYFLCAPRLESHLEPGSKKSFLRLASLLEDLELLGGDKLTFRLHLLTTIGRADLVKNLQV

>KS orfk13A
TYEVLCEVARKLGTDDREVVLFLNVFLPQPTLAQLIGALRALKEEGRLTFPLAECLPRAGRDLRLDLH

>KS orfk13B
YQLTVLHVDGELCARDYRSLIFLSKDTIGSRSTPQTFELHNVYCMENLDLLGPTDVDALMSMLRSLSRVDLQRQVQT

>HIP1
SELEADLAEQQHLRQQAADDCEFLRAELDELRRQREDTEKAQRSLSIEIERKAQANEQRYSKLKEKYSELVQNHADLLRKN
AE

>HIP1a
GELEEQRKQKQKALVDNEQLRHELAQLRAAQLERERSQGLREEAERKASATEARYNKLKEKHSSELVHVHAEELLRKNAD

>mHIP1a
NGLEAELEEQRKQKQKALVDNEQLRHELAQLKALQLEGARNQGLREEAERKASATEARYSKLKEKHSSELINTHAEELLRKN
AD

>mHIP1
SELEAELEQQHLGRQAMDDCEFLRTELDELKRQREDTEKAQRSLTEIERKAQANEQRYSKLKEKYSELVQNHADLLRKN
AE

Genetic map of 7q11.23

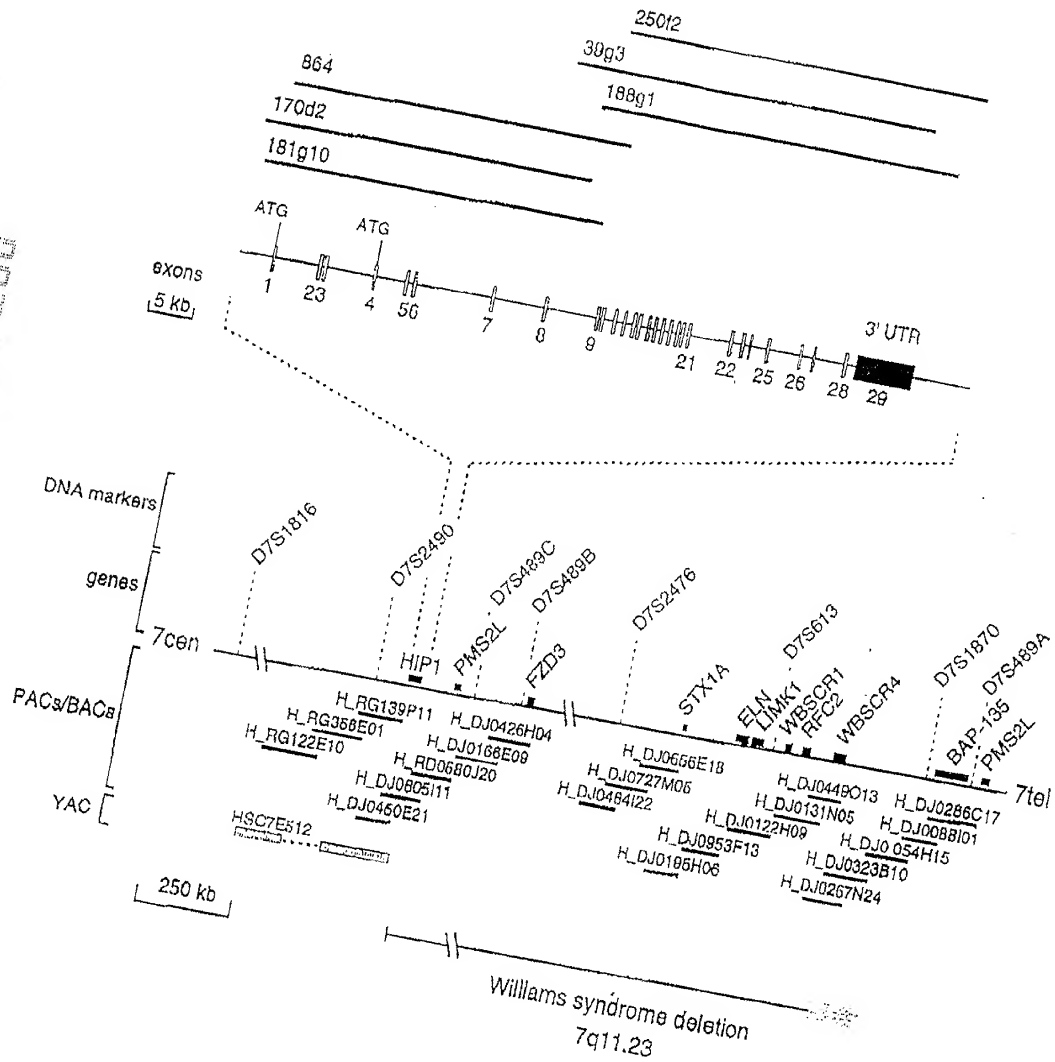


Fig 5

Fig 2

1 hip1 MLQCSBHRDQQL GTANARQWCPPLPPA GRLOCTDHPWGWRL AGGGERGLMEGLSH SORLIHLILLSLPL 90
2 zk370.3 -----MDHQAQAREVFV 12

1 hip1 Q KAI E . . K KHART I . GT E KK FW V L VL WKECH . HLLRDGEP V RY N S 180
2 zk370.3 VQTVSINKAINTQ3 VAVREKHARTCILGT HSEKGAQTFWVVR LPLSSNAVLCWKECH VFHKLRLDGHNVLK DSLRYBN3LSDMRH 102
RAQLEAVQKAITQNE VPLKPRHARTITVGT HSEKSSGTFWTVGR IQLRHPTLWKECH LVHKLRLDGHGRV96 ETRYVVRRTQLSQP

1 hip1 W HL GYG Y KLL . H K P PG L D QL X D . N F T M L V . R S . 269
2 zk370.3 WKHLNTSGYGPICIES YCKLHDRVTFENKY PVVPGKLDLNDSQLK TL-EGDLNDFETII DLILDQDALLVQLDR VYERQNSLRWNSLIP 191

1 hip1 GQC PLI . ILO S YDY VK . PKL HS . D L G ER RF P K . SSNLTFFK L . IL LP PNEL S 355
2 zk370.3 AGQCLAPLIQVILQ CSHLYDYTVKLLPKL HSCLP-----ADTLQG HRDRFNRQFTLKDOL FYRSMNLTQFKRLIQ IPQDPENPPNFRAS 277
QGOCHLSPLIIAIIID TSKEFYDYLKMIKUL HSOVP-----PDALSG HRSNFTIPTERTKXF YEESNMLTQFKYLVS IPTTESHAPNTLOQS

1 hip1 L P E S D H D D I L . K E 445
2 zk370.3 ALSEHISPVVVIPIAE ASSPDSEPVLEKDDOL MDWDASQQM.FDNKF DDIFGSSPSSDPFNF NSQNGWKNDEKNDHLI ERLYREISGLKAQLE 346
DLESYRTPHAYLHSE GS-----E-----DGTSLHGHDGEL LNLAEAPQO--ASP SSQ-----PDPRREQI VMLSRVAVDEKFAKE

1 hip1 E . Q L E R T A . E ERKA A E R K K Y 530
2 zk370.3 NMKTES---QRVLQ LKGVSELEADLAEQ QHLRQQAADCEFLR AELDELRQRREDTEX AQRSSEIERAKAQN HQ-RYSKLLKKTSE- 429
RLIQ3A---RSRIEQ YENRLLQWQGEFDHA KREADENRBEAQRLEK NELALRDASRTQIDD AR--VIERAEIKATAA EE-RFNKKGGVTEK-

1 hip1 H L KQ. D L QR S 617
2 zk370.3 ---LVQNEADLLRN ARVTQVSMARQAV DLERKXKLEDSLER ISDQGRKTOEQLEV LESLKOELATSQREL QVLQGSLETSFQSEA 498
---PRSEVLALTKL GDIOZQLEASZSKS? DRDEZ-----ITALNR KVERAQR-----BAGRALTKA EGDAGVDEMRTOLV

1 hip1 E EL D H E Q AX . E Q A P 702
2 zk370.3 WRAEFAELKBRDS LVSGAAHRRBBSLAL RKELQDTQLKLASTE ESMCQLAKDQRHLL VGSRRARQVIODAL MOLEFPPLIS----- 569
KADIEVBEIKRTID- -----ELRESHAN- -QLVQSSNEBTNKIR LBELEVAKES-GYUL TQMEDHCEDALQVAT SITYPF-----

1 hip1 HL I E L A HL S A A CK A 792
2 zk370.3 CAGSADHLILSVTSI SSCIEQLEKSWQYL ACPSDISGULLHSITL LAHLTSDALNHGATT CLRAPPPADSLTBA CKQYGRETLAYLASL 641
-----HLAQSAMH! LVNLSNER-LDEPL ATQDNV-----F AGHLSTILLSAASA AYTASIRSVEGVNDQ CEKV---LAAAKVAF

1 hip1 L D LP DI . EM AI A IE RA G LEVNE IL 882
2 zk370.3 EEEGLENADSTANR NCLSKIKAIAGEELLIP RGDIKQBELGLDLYD KEMARTSAAYETATA RIBEMLSRAGDTG VKLEVNRIIGCOCTS 731
SDDSALSRADKAKILL RQDIQIENSLHISLP LQIDIDIXVGVNELE QEMRRMDAIRRAVQ BIEAIQRRARESSDG IRLEVNESILANCOA

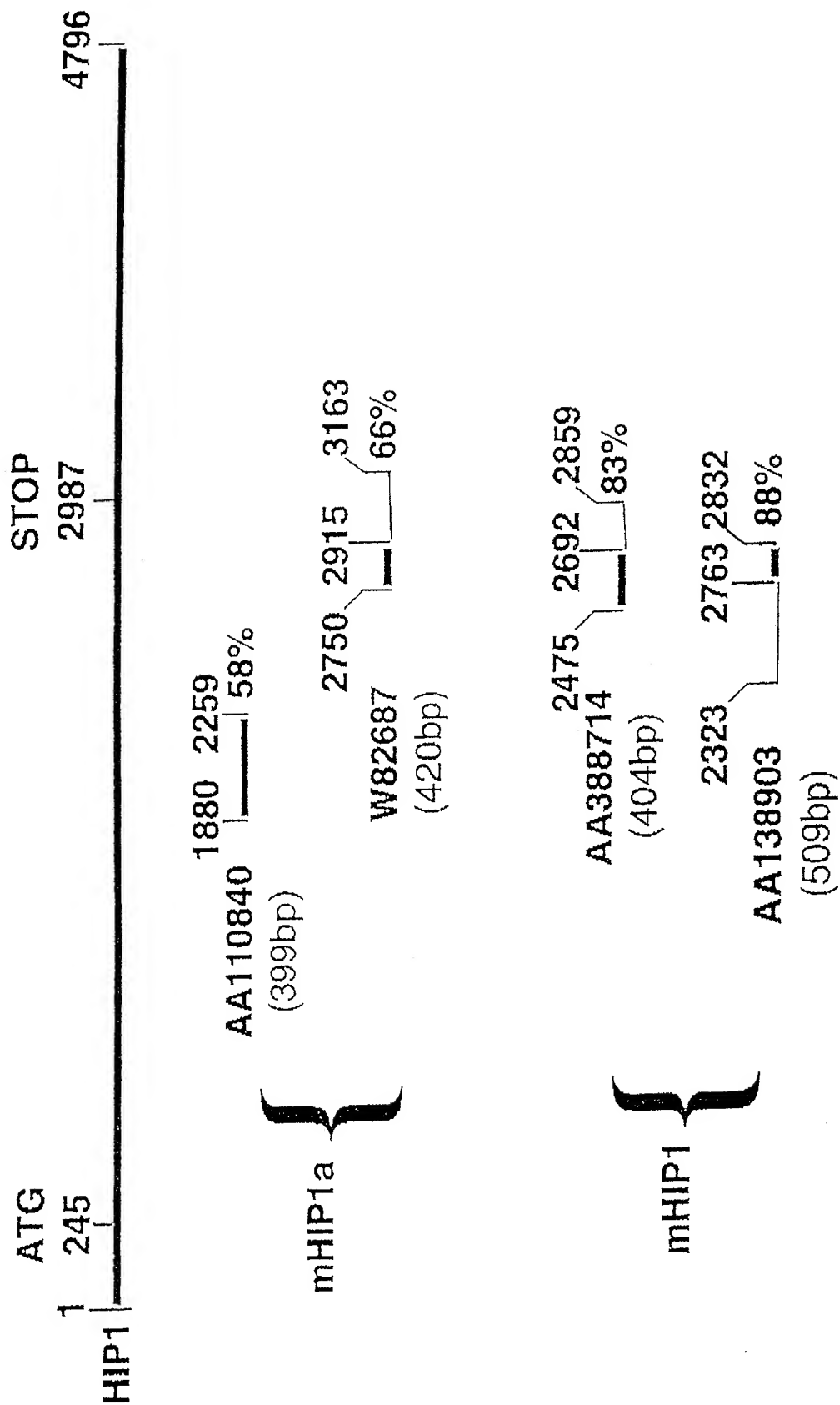
FIG 2 (CONT.)

EM . I . L . . AS	L Q EIV	SP	EZY N	NTGLIS A	KAVQ A V V	AD VV	GRKK F E L Y	EIAASTA	
1 hip1	LMQAIQVLLIVASKDL	QREIVESGRGTASPK	EZYAKNSHTSGLIS	ASKAVHGKNTWYDA	ADLVYQGRK-----F	KELATVCSH	EIAASTA	969	
2 2k370.3	LMSVIMQVLVIASREL	QTEIVAAGKGGSPA	EZYERHQHTSGLIS	AAKAVGVAARVIVES	ADGWATGKI-----F	EHLIVARQZ	EIAASTA	917	
	QL . S VKADKSS	L L A	VHQ TA VVA	G .	DZS L	K ER SQV L	ELK L	ER EL	
1 hip1	QLVAASKVKAADNDSP	NLAQIQQASRGYNQA	TAGVVASTISGKSQI	BETDM--MDPSSMTL	TQIKRQEDSQVKVL	ELENKLOQERQ	KMLKK	1056	
2 2k370.3	QLEVESSEPVKADKSS	KIDALSVAARKVQN	TROVVAVYKNGQTTL	NDEGS--LDPSTYLSL	HAAKKEESQVYKHL	HUBQSLNQERK	KLAA	505	
	LRK HY A .								
1 hip1	LRKKHYELAGVAGWG	EEGTASAPPTLQEVV	TEKE	1090					
2 2k370.3	LRKQHYEPAQLVANK	VSP-----	----	923					

Fig 7

Fig 7

Mouse ESTs



Hip-1 increases the susceptibility to cell stress

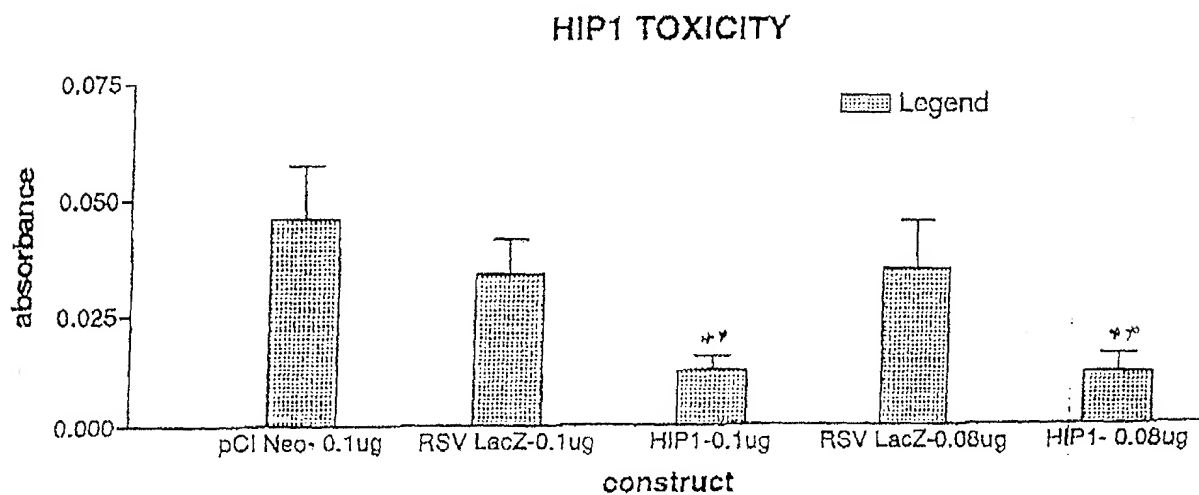


Fig 8

Hip-1 is toxic in the presence of huntingtin

HIP1 transfected into HD1955-15 stable cell line
36 hr post-transfection

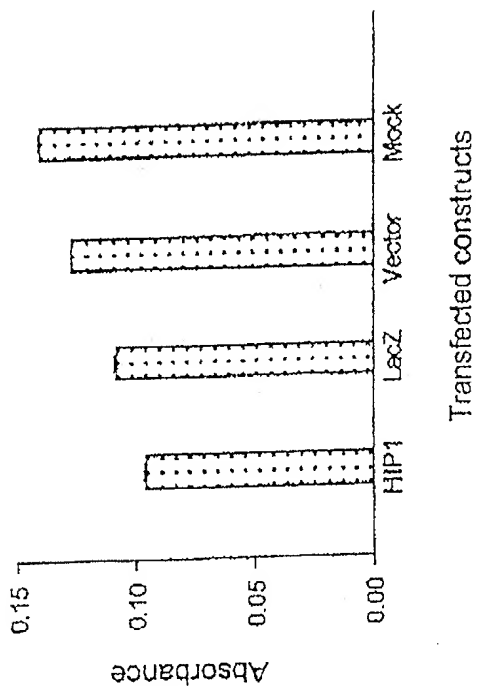


Fig 9A

Hip-1 is toxic in the presence of huntingtin

HIP1 transfected into HD1955-128 stable cell line
36 hr post-transfection

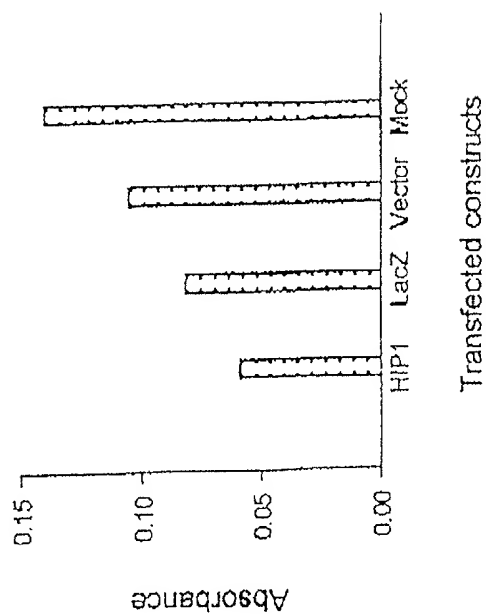
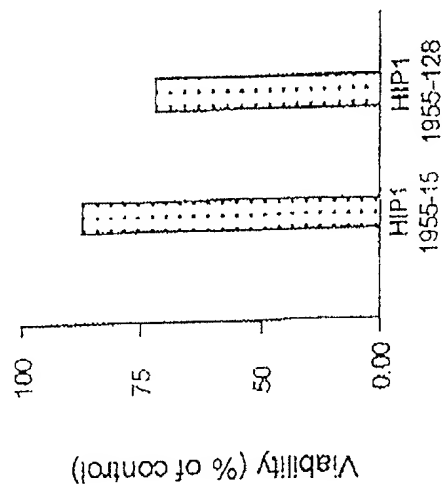


Fig 9B

Polyglutamine-dependence of HIP-1 toxicity



Transfected constructs/cell lines

Fig 9c